

6. Ewoldt

ENTERED



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/582,340A

DATE: 09/12/2002

TIME: 13:50:24

Input Set : A:\255-013.st25.txt

Output Set: N:\CRF4\09122002\I582340A.raw

3 <110> APPLICANT: Institute National De La Sante Et De La Recherche Medicale
 4 Raposo, Graca
 5 Thery, Clotilde
 6 Amigorena, Sebastian
 8 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS USING LACTADHERIN OR VARIANTS
 THEREOF

10 <130> FILE REFERENCE: 255/013 KTM
 12 <140> CURRENT APPLICATION NUMBER: US 09/582,340A
 13 <141> CURRENT FILING DATE: 1999-11-23
 15 <160> NUMBER OF SEQ ID NOS: 6
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1934
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (61)..(1224)
 27 <223> OTHER INFORMATION:
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 33 atg ccg cgc ccc cgc ctg ctg gcc gcg ctg tgc ggc gcg ctg ctc tgc 108
 34 Met Pro Arg Pro Arg Leu Leu Ala Ala Leu Cys Gly Ala Leu Leu Cys
 35 1 5 10 15
 37 gcc ccc agc ctc ctc gtc gcc ctg gat atc tgt tcc aaa aac ccc tgc 156
 38 Ala Pro Ser Leu Leu Val Ala Leu Asp Ile Cys Ser Lys Asn Pro Cys
 39 20 25 30
 41 cac aac ggt ggt tta tgc gag gag att tcc caa gaa gtg cga gga gat 204
 42 His Asn Gly Gly Leu Cys Glu Glu Ile Ser Gln Glu Val Arg Gly Asp
 43 35 40 45
 45 gtc ttc ccc tcg tac acc tgc acg tgc ctt aag ggc tac gcg ggc aac 252
 46 Val Phe Pro Ser Tyr Thr Cys Thr Cys Leu Lys Gly Tyr Ala Gly Asn
 47 50 55 60
 49 cac tgt gag acg aaa tgt gtc gag cca ctg ggc atg gag aat ggg aac 300
 50 His Cys Glu Thr Lys Cys Val Glu Pro Leu Gly Met Glu Asn Gly Asn
 51 65 70 75 80
 53 att gcc aac tca cag atc gcc gcc tca tct gtg cgt gtg acc ttc ttg 348
 54 Ile Ala Asn Ser Gln Ile Ala Ala Ser Ser Val Arg Val Thr Phe Leu
 55 85 90 95
 57 ggt ttg cag cat tgg gtc ccg gag ctg gcc cgc ctg aac cgc gca ggc 396
 58 Gly Leu Gln His Trp Val Pro Glu Leu Ala Arg Leu Asn Arg Ala Gly
 59 100 105 110
 61 atg gtc aat gcc tgg aca ccc agc agc aat gac gat aac ccc tgg atc 444
 62 Met Val Asn Ala Trp Thr Pro Ser Ser Asn Asp Asp Asn Pro Trp Ile

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65	cag gtg aac ctg ctg cgg agg atg tgg gta aca ggt gtg gtg acg cag	492		
66	Gln Val Asn Leu Leu Arg Arg Met Trp Val Thr Gly Val Val Thr Gln			
67	130	135	140	
69	ggt gcc agc cgc ttg gcc agt cat gag tac ctg aag gcc ttc aag gtg	540		
70	Gly Ala Ser Arg Leu Ala Ser His Glu Tyr Leu Lys Ala Phe Lys Val			
71	145	150	155	160
73	gcc tac agc ctt aat gga cac gaa ttc gat ttc atc cat gat gtt aat	588		
74	Ala Tyr Ser Leu Asn Gly His Glu Phe Asp Phe Ile His Asp Val Asn			
75	165	170	175	
77	aaa aaa cac aag gag ttt gtg ggt aac tgg aac aaa aac gcg gtg cat	636		
78	Lys Lys His Lys Glu Phe Val Gly Asn Trp Asn Lys Asn Ala Val His			
79	180	185	190	
81	gtc aac ctg ttt gag acc cct gtg gag gct cag tac gtg aga ttg tac	684		
82	Val Asn Leu Phe Glu Thr Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr			
83	195	200	205	
85	ccc acg agc tgc cac acg gcc tgc act ctg cgc ttt gag cta ctg ggc	732		
86	Pro Thr Ser Cys His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly			
87	210	215	220	
89	tgt gag ctg aac gga tgc gcc aat ccc ctg ggc ctg aag aat aac agc	780		
90	Cys Glu Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn Ser			
91	225	230	235	240
93	atc cct gac aag cag atc acg gcc tcc agc agc tac aag acc tgg ggc	828		
94	Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys Thr Trp Gly			
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97	ttg cat ctc ttc agc tgg aac ccc tcc tat gca cgg ctg gac aag cag	876		
98	Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala Arg Leu Asp Lys Gln			
99	260	265	270	
101	ggc aac ttc aac gcc tgg gtt gcg ggg agc tac ggt aac gat cag tgg	924		
102	Gly Asn Phe Asn Ala Trp Val Ala Gly Ser Tyr Gly Asn Asp Gln Trp			
103	275	280	285	
105	ctg cag gtg gac ctg ggc tcc tcg aag gag gtg aca ggc atc atc acc	972		
106	Leu Gln Val Asp Leu Gly Ser Lys Glu Val Thr Gly Ile Ile Thr			
107	290	295	300	
109	cag ggg gcc cgt aac ttt ggc tct gtc cag ttt gtg gca tcc tac aag	1020		
110	Gln Gly Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys			
111	305	310	315	320
113	gtt gcc tac agt aat gac agt gcg aac tgg act gag tac cag gac ccc	1068		
114	Val Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro			
115	325	330	335	
117	agg act ggc agc agt aag atc ttc cct ggc aac tgg gac aac cac tcc	1116		
118	Arg Thr Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His Ser			
119	340	345	350	
121	cac aag aag aac ttg ttt gag acg ccc atc ctg gct cgc tat gtg cgc	1164		
122	His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg Tyr Val Arg			
123	355	360	365	
125	atc ctg cct gta gcc tgg cac aac cgc atc gcc ctg cgc ctg gag ctg	1212		
126	Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala Leu Arg Leu Glu Leu			
127	370	375	380	

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129 ctg ggc tgt tag tggccacctg ccacccccag gtcttcctgc tttccatggg      1264
130 Leu Gly Cys
131 385
133 cccgctgcct cttggcttct cagccccctt aaatcaccat agggctgggg actggggaag      1324
135 gggagggtgt tcagaggcag caccaccaca cagtcacccc tccctccctc tttcccaccc      1384
137 tccacctctc acggggccctg ccccagcccc taagccccgt cccctaacc cagtcctca      1444
139 ctgtcctgtt ttcttaggca ctgagggatc tgagtaggtc tgggatggac aggaaagggc      1504
141 aaagttagggc gtgtggtttc cctgccccctg tccggaccgc cgatcccagg tgcgtgtgtc      1564
143 tctgtctctc ctagccccctc tctcacacat cacattccca tgggtggcctc aagaaaaggcc      1624
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147 taccatgtgc cacaactgct gtggccccct gtccccaaga cacttccctc tgtctccctg      1744
149 gttgcctctc ttgccccttg tctgaagcc cagcgacaca gaagggggtg gggcggtgtc      1804
151 atggggagaa agggagcgag gtcagaggag ccggcatggg ttggcagggt gggcggtgtg      1864
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155 tcttcacggg      1934
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159 <211> LENGTH: 387
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169 Ala Pro Ser Leu Leu Val Ala Leu Asp Ile Cys Ser Lys Asn Pro Cys
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173 His Asn Gly Gly Leu Cys Glu Glu Ile Ser Gln Glu Val Arg Gly Asp
174 35 40 45
177 Val Phe Pro Ser Tyr Thr Cys Thr Cys Leu Lys Gly Tyr Ala Gly Asn
178 50 55 60
181 His Cys Glu Thr Lys Cys Val Glu Pro Leu Gly Met Glu Asn Gly Asn
182 65 70 75 80
185 Ile Ala Asn Ser Gln Ile Ala Ala Ser Ser Val Arg Val Thr Phe Leu
186 85 90 95
189 Gly Leu Gln His Trp Val Pro Glu Leu Ala Arg Leu Asn Arg Ala Gly
190 100 105 110
193 Met Val Asn Ala Trp Thr Pro Ser Ser Asn Asp Asp Asn Pro Trp Ile
194 115 120 125
197 Gln Val Asn Leu Leu Arg Arg Met Trp Val Thr Gly Val Val Thr Gln
198 130 135 140
201 Gly Ala Ser Arg Leu Ala Ser His Glu Tyr Leu Lys Ala Phe Lys Val
202 145 150 155 160
205 Ala Tyr Ser Leu Asn Gly His Glu Phe Asp Phe Ile His Asp Val Asn
206 165 170 175
209 Lys Lys His Lys Glu Phe Val Gly Asn Trp Asn Lys Asn Ala Val His
210 180 185 190
213 Val Asn Leu Phe Glu Thr Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr
214 195 200 205
217 Pro Thr Ser Cys His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly
218 210 215 220
221 Cys Glu Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn Ser

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222 225          230          235          240
225 Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys Thr Trp Gly
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229 Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala Arg Leu Asp Lys Gln
230          260          265          270
233 Gly Asn Phe Asn Ala Trp Val Ala Gly Ser Tyr Gly Asn Asp Gln Trp
234          275          280          285
237 Leu Gln Val Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr
238          290          295          300
241 Gln Gly Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys
242 305          310          315          320
245 Val Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro
246          325          330          335
249 Arg Thr Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His Ser
250          340          345          350
253 His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg Tyr Val Arg
254          355          360          365
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266 <211> LENGTH: 2077
267 <212> TYPE: DNA
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273 <223> OTHER INFORMATION:
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281 cgt gtg ctg gcc gcg ctg tgc ggc atg cta ctc tgc gcc tct ggc ctc      105
282 Arg Val Leu Ala Ala Leu Cys Gly Met Leu Leu Cys Ala Ser Gly Leu
283 5          10          15          20
285 ttc gcc gcg tct ggt gac ttc tgt gac tcc agc ctg tgc ctg aac ggt      153
286 Phe Ala Ala Ser Gly Asp Phe Cys Asp Ser Ser Leu Cys Leu Asn Gly
287          25          30          35
289 ggc acc tgc ttg acg ggc caa gac aat gac atc tac tgc ctc tgc cct      201
290 Gly Thr Cys Leu Thr Gly Gln Asp Asn Asp Ile Tyr Cys Leu Cys Pro
291          40          45          50
293 gaa ggc ttc aca ggc ctt gtg tgc aat gag act gag aga gga cca tgc      249
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295          55          60          65
297 tcc cca aac cct tgc tac aat gat gcc aaa tgt ctg gtg act ttg gac      297
298 Ser Pro Asn Pro Cys Tyr Asn Asp Ala Lys Cys Leu Val Thr Leu Asp
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301 aca cag cgt ggg gac atc ttc acc gaa tac atc tgc cag tgc cct gtg      345

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302	Thr	Gln	Arg	Gly	Asp	Ile	Phe	Thr	Glu	Tyr	Ile	Cys	Gln	Cys	Pro	Val	
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306	Gly	Tyr	Ser	Gly	Ile	His	Cys	Glu	Thr	Glu	Thr	Asn	Tyr	Tyr	Asn	Leu	
307					105					110					115		
309	gat	gga	gaa	tac	atg	ttc	acc	aca	gcc	gtc	ccc	aat	act	gcc	gtc	ccc	441
310	Asp	Gly	Glu	Tyr	Met	Phe	Thr	Thr	Ala	Val	Pro	Asn	Thr	Ala	Val	Pro	
311				120					125					130			
313	acc	ccg	gcc	ccc	acc	ccc	gat	ctt	tcc	aac	aac	cta	gcc	tcc	cgt	tgt	489
314	Thr	Pro	Ala	Pro	Thr	Pro	Asp	Leu	Ser	Asn	Asn	Leu	Ala	Ser	Arg	Cys	
315			135					140					145				
317	tct	aca	cag	ctg	ggc	atg	gaa	ggg	ggc	gcc	att	gct	gat	tca	cag	att	537
318	Ser	Thr	Gln	Leu	Gly	Met	Glu	Gly	Gly	Ala	Ile	Ala	Asp	Ser	Gln	Ile	
319		150					155					160					
321	tcc	gcc	tcg	tat	gtg	tat	atg	ggt	ttc	atg	ggc	ttg	cag	cgc	tgg	ggc	585
322	Ser	Ala	Ser	Tyr	Val	Tyr	Met	Gly	Phe	Met	Gly	Leu	Gln	Arg	Trp	Gly	
323	165				170					175					180		
325	ccg	gag	ctg	gct	cgt	ctg	tac	cgc	aca	ggg	atc	gtc	aat	gcc	tgg	cac	633
326	Pro	Glu	Leu	Ala	Arg	Leu	Tyr	Arg	Thr	Gly	Ile	Val	Asn	Ala	Trp	His	
327					185					190					195		
329	gcc	agc	aac	tat	gat	agc	aag	ccc	tgg	atc	cag	gtg	aac	ctt	ctg	cgg	681
330	Ala	Ser	Asn	Tyr	Asp	Ser	Lys	Pro	Trp	Ile	Gln	Val	Asn	Leu	Leu	Arg	
331			200					205						210			
333	aag	atg	cgg	gta	tca	ggt	gtg	atg	acg	cag	ggt	gcc	agc	cgt	gcc	ggg	729
334	Lys	Met	Arg	Val	Ser	Gly	Val	Met	Thr	Gln	Gly	Ala	Ser	Arg	Ala	Gly	
335			215					220					225				
337	agg	gcg	gag	tac	ctg	aag	acc	ttc	aag	gtg	gct	tac	agc	ctc	gac	gga	777
338	Arg	Ala	Glu	Tyr	Leu	Lys	Thr	Phe	Lys	Val	Ala	Tyr	Ser	Leu	Asp	Gly	
339		230					235					240					
341	cgc	aag	ttt	gag	ttc	atc	cag	gat	gaa	agc	ggt	gga	gac	aag	gag	ttt	825
342	Arg	Lys	Phe	Glu	Phe	Ile	Gln	Asp	Glu	Ser	Gly	Gly	Asp	Lys	Glu	Phe	
343	245					250					255				260		
345	ttg	ggt	aac	ctg	gac	aac	aac	agc	ctg	aag	gtt	aac	atg	ttc	aac	ccg	873
346	Leu	Gly	Asn	Leu	Asp	Asn	Asn	Ser	Leu	Lys	Val	Asn	Met	Phe	Asn	Pro	
347					265					270					275		
349	act	ctg	gag	gca	cag	tac	ata	agg	ctg	tac	cct	gtt	tcg	tgc	cac	cgc	921
350	Thr	Leu	Glu	Ala	Gln	Tyr	Ile	Arg	Leu	Tyr	Pro	Val	Ser	Cys	His	Arg	
351				280					285					290			
353	ggc	tgc	acc	ctc	cgc	ttc	gag	ctc	ctg	ggc	tgt	gag	ttg	cac	gga	tgt	969
354	Gly	Cys	Thr	Leu	Arg	Phe	Glu	Leu	Leu	Gly	Cys	Glu	Leu	His	Gly	Cys	
355			295					300					305				
357	ctc	gag	ccc	ctg	ggc	ctg	aag	aat	aac	aca	att	cct	gac	agc	cag	atg	1017
358	Leu	Glu	Pro	Leu	Gly	Leu	Lys	Asn	Asn	Thr	Ile	Pro	Asp	Ser	Gln	Met	
359		310					315					320					
361	tca	gcc	tcc	agc	agc	tac	aag	aca	tgg	aac	ctg	cgt	gct	ttt	ggc	tgg	1065
362	Ser	Ala	Ser	Ser	Ser	Tyr	Lys	Thr	Trp	Asn	Leu	Arg	Ala	Phe	Gly	Trp	
363	325					330					335				340		
365	tac	ccc	cac	ttg	gga	agg	ctg	gat	aat	cag	ggc	aag	atc	aat	gcc	tgg	1113
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